



# STIC Search Report

## Biotech-Chem Library

10/042059  
File Copy  
updated

STIC Database Tracking Number: 146941

**TO: David Lamberston**  
**Location: rem/2b79/2c70**  
**Wednesday, April 13, 2005**  
**Art Unit: 1636**  
**Serial Number: 10/042059**

**From: Beverly Shears**  
**Location: Biotech-Chem Library**  
**REM 1A54**  
**Phone: 571-272-2528**  
**beverly.shears@uspto.gov**

### Search Notes

From: Lambertson, David  
Sent: Tuesday, April 05, 2005 1:43 PM  
To: STIC-Biotech/ChemLib  
Cc: Lambertson, David  
Subject: Search Request

## Search Request

Examiner's Name:	David Lambertson
Examiner #:	79514
Art Unit:	1636
Room #:	Remsen 02B79
Mailbox room#:	Remsen 02C70
Phone:	(571) 272-0771
Results Format:	paper

Serial # 10/042059

Please Search:

Nucleic Acid databases for:

SEQ ID NO: 1

Including:

1. Oligo Search.

Thanks,  
Dave.

1-843 N/A  
LB

4/5/05

Date completed:

Searcher: Beverly e 2528

Terminal time: \_\_\_\_\_

Elapsed time: \_\_\_\_\_

CPU time: \_\_\_\_\_

Total time: \_\_\_\_\_

Number of Searches: \_\_\_\_\_

Number of Databases: \_\_\_\_\_

### Search Site

\_\_\_\_\_ STIC

\_\_\_\_\_ CM-1

\_\_\_\_\_ Pre-S

### Type of Search

\_\_\_\_\_ N.A. Sequence

\_\_\_\_\_ A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

### Vendors

\_\_\_\_\_ IG

\_\_\_\_\_ STN

\_\_\_\_\_ Dialog

\_\_\_\_\_ APS

\_\_\_\_\_ Geninfo

\_\_\_\_\_ SDC

\_\_\_\_\_ DARC/Questel

☒ Other CGN

GenCore version 5.1.6  
(c) 1993 - 2005 Compu

Search time 4116 Seconds  
(without alignments)  
9924.137 Million cell up

.....tctcctctgg

residues

**Parameters:**

3

redicted by char  
score of the resu  
al score distri

## SE

	Description
BD266599	Nucleic acid
AK043378	Sequence
AF204738	Pichia pastoris
BD266600	Nucleic acid
AK043760	Sequence
Continuation (21 of 21)	
Continuation (21 of 21)	
AR548979	Sequence
Continuation (2 of 2)	
M24517	Saccharomyces cerevisiae
249219	S. cerevisiae
Z71355	S. cerevisiae
AY693179	Saccharomyces cerevisiae
Continuation (8 of 12)	
Continuation (12 of 12)	
BD178335	Transferrin
AB116236	Roseallium
AK105512	Oryza sativa
AR404667	Sequence

C	20	131.4	15.6	1250	8	AK06898431
	21	113.6	13.5	3167	8	AF13329413
	22	111.2	13.2	1223	6	AR4046668
	23	110	13.0	1000	8	LA7356
	24	107.6	12.8	951	8	ET005306
	25	107.6	12.8	1143	8	AK117860
	26	104.4	12.4	1217	6	AR2366359
C	27	104.4	12.4	1217	6	AR2366413
	28	104.4	12.4	1217	6	AX465676
C	29	104.4	12.4	1217	6	AX464508
	30	104.4	12.4	1217	8	AF131219
	31	100.6	11.9	11000	2	AP006499
	32	99.8	11.8	1020	6	AR4046888
	33	97.4	11.6	798	6	AX5062777
	34	97.4	11.6	829	8	AY1338404
	35	97.4	11.6	893	6	AX333935
	36	97.4	11.6	929	6	AR236633
C	37	97.4	11.6	1006	6	AR236640
	38	97.4	11.6	1006	6	AX343933
	39	97.4	11.6	1006	6	AX4657575
C	40	97.4	11.6	1006	6	AX464581
	41	97.4	11.6	1006	8	LA7355
	42	97.4	11.6	1055	8	AY065238
	43	93.6	11.1	1205	6	AX5060427
	44	93.6	11.1	1207	6	AR236633
C	45	93.6	11.1	1207	6	AR236639

“

RESULT 1	
BD266599	843
LOCUS	
DEFINITION	Nucleic acid molecule, contai
ACCESSION	polypeptide with chorismate m
VERSION	BD266599
KEYWORDS	BD266599.1 GI:33076367
SOURCE	JP 2002542788-A/1.
ORGANISM	Pichia angusta
	Pichia angusta
	Eukaryota; Fungi; Ascomycota;:
REFERENCE	Saccharomycetales; Saccharomy
AUTHORS	1 (bases 1 to 843)
TITLE	Gellissen,G., Braus,G., Pries
JOURNAL	Nucleic acid molecule, contai
	polypeptide with chorismate m
	Patent: JP 2002542788-A 1 17-7
	RHEIN-BIOTECH GESSELLSCHAFT FU
	PRODUKTE MBH
COMMENT	OS Hansenula polymorpha (ye
	PN JP 2002542788-A/1
	PD 17-DEC-2002
	PF 27-APR-2000 JP 200061446
	PI 27-APR-1999 DE 199 19 12
	PI GERD GELLISSEN, GERHARD B
	ALEXANDER W STRASSER
	PC C12N15/09, C07K16/40, C12N
	, C12N9/90, C12N15/00,
	PC C12N5/00
	CC Nucleic acid molecule, c
	CC for a
	CC polypeptide with chorism
	PH key
	FT source
FEATURES	Location/Qualifiers
SOURCE	1..843
ORIGIN	/organism="Pichia angusta" /mol_type="genomic DNA" /db_xref="taxon:4905"

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OM nucleic - nucleic search, using ew model

Run on: April 9, 2005, 18:36:30 ; Search time 586 Seconds  
(without alignments)  
8515.942 Million cell updates/sec

Title: US-10-042-059B-1

Perfect score: 843  
Sequence: 1 atgcagcttatgaagccagca.....tctcctcgtcgtctgactag 843

Scoring table: IDENTITY NTC  
Gapop 10\_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_16Dec04:\*  
1: geneseqn19808:\*  
2: geneseqn19908:\*  
3: geneseqn20008:\*  
4: geneseqn20018:\*  
5: geneseqn20018:\*  
6: geneseqn20028:\*  
7: geneseqn20038:\*  
8: geneseqn20038:\*  
9: geneseqn20038:\*  
10: geneseqn20038:\*  
11: geneseqn20038:\*  
12: geneseqn20048:\*  
13: geneseqn20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	843	100.0	843	3	AAC81949
2	843	100.0	1655	3	AAC81950
3	270	32.0	807	12	ADP98547
4	182.8	21.7	801	13	ADR85510
5	156.4	18.6	869	8	AA550282
6	141.2	16.7	989	13	ADR84923
7	141.2	16.7	2920	8	ABT17891
8	141.2	16.7	2987	8	ABT17891
9	141.2	16.7	6989	13	ADR84336
10	131.4	15.6	1231	10	ABX93057
11	131.4	15.6	1231	12	ADJ55263
12	116.8	13.9	658	3	AA14469
13	111.2	13.2	1223	10	ABX93056
14	111.2	13.2	1223	12	ADJ55261
15	104.4	12.4	1317	6	ABA91395
16	104.4	12.4	1317	6	ABA91401
17	99.8	11.8	1020	10	ABX93058
18	99.8	11.8	1020	12	ADJ55265
19	97.4	11.6	798	6	AB213167
20	97.4	11.6	993	6	ABA99614

21	97.4	11.6	1006	6	ABA99613
22	97.4	11.6	1006	6	ABA91400
23	97.4	11.6	1006	6	ABA91394
24	93.6	11.1	1005	6	AB212932
25	93.6	11.1	1207	6	ABA91393
26	93.6	11.1	1207	6	ABA91399
27	93.6	11.1	1274	3	AAC33324
28	73	8.7	580	13	ACN57510
29	69.8	8.3	622	13	ACN50132
30	64.2	7.6	600	13	ADR64815
31	61.8	7.3	258	6	AB171526
32	61	7.2	780	10	ABX93059
33	61	7.2	780	12	ADJ55267
34	59.8	7.1	579	10	ABX93054
35	59.8	7.1	579	12	ADJ55257
36	56.2	6.7	584	13	ACN50205
37	54.8	6.5	542	13	ACN57601
38	53.4	6.3	525	10	ABX93053
39	53.4	6.3	525	12	ADJ55255
40	52.6	6.2	524	13	ADR64235
41	49.4	5.9	2000	8	ADA71938
42	48.8	5.8	864	12	ADU44958
43	47.6	5.6	1379	6	ABA91794
44	47	5.6	5858	8	ADJ55726
45	46.8	5.6	180385	10	ADL13931

#### ALIGNMENTS

RESULT 1		
ID	AAC81949	strand: DNA, 843 BP.
AC	AAC81949;	
DT	15-SEP-2003	(revised)
DT	01-MAR-2001	(first entry)
DE	H. polymorpha chorismate mutase DNA.	
KW	Chorismate mutase; prephenate; selection marker; auxotrophic yeast; ds.	
OS	Pichia angusta.	
PN	WO200065071-A1.	
XX	02-NOV-2000.	
XX	27-APR-2000; 2000WO-EP003844.	
XX	27-APR-1999; 99DE-01019124.	
XX	(RHEI-) RHEIN BIOTECH GES NEUE BIOTECHNOLOGISCHE.	
XX	Gellissen G, Braus G, Pries R, Krappmann S, Strasser AM;	
XX	WPI: 2000-687355/67.	
XX	P-PSDB; AAB11451.	
PT	Nucleic acids encoding chorismate mutase, useful for preparing an	
PT	auxotrophic selection system for recombinant yeast and for recombinant	
PT	protein expression.	
PS	Claim 1a; Page 57; 63pp; German.	
CC	This invention describes novel nucleic acids (I) that encode a	
CC	polypeptide (II) with chorismate mutase (CM) activity (or its	
CC	complementary strand). CM catalyzes conversion of chorismate to	
CC	prephenate, an essential precursor for Phe and Tyr. (I) is a selection	
CC	marker for construction of corresponding auxotrophic yeast (requiring Phe	
CC	and Tyr) that are used for recombinant production of proteins. (I) allows	
CC	selection of transformed yeast on simple media. (Updated on 15-SEP-2003	

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OM nucleic - nucleic search, using SW model

Run on: April 9, 2005, 19:49:42 ; Search time 193 Seconds  
(without alignments)  
7147.053 Million cell updates/sec

Title: US-10-042-059b-1

Sequence: 1 atggaattatgaagcagcaga.....ctccctctgctgctag 843

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/prodata/1/ina/backfillseq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	270	32.0	948	4	US-09-248-796A-4110 Sequence 4110, Ap
2	131.4	15.6	1231	4	US-09-454-279-13 Sequence 13, Appl
3	111.2	13.2	1223	4	US-09-454-279-11 Sequence 11, Appl
4	104.4	12.4	1217	3	US-09-610-040-4 Sequence 4, Appl
5	104.4	12.4	1217	3	US-09-610-040-10 Sequence 10, Appl
6	104.4	12.4	1217	4	US-10-267-763-4 Sequence 4, Appl
7	104.4	12.4	1217	4	US-10-267-763-10 Sequence 10, Appl
8	99.8	11.8	1020	4	US-09-454-279-15 Sequence 15, Appl
9	97.4	11.6	1006	3	US-09-610-040-3 Sequence 3, Appl
10	97.4	11.6	1006	3	US-09-610-040-9 Sequence 9, Appl
11	97.4	11.6	1006	4	US-10-267-763-3 Sequence 3, Appl
12	97.4	11.6	1006	4	US-10-267-763-9 Sequence 9, Appl
13	93.6	11.1	1207	3	US-09-610-040-2 Sequence 2, Appl
14	93.6	11.1	1207	3	US-09-610-040-8 Sequence 8, Appl
15	93.6	11.1	1207	4	US-10-267-763-2 Sequence 2, Appl
16	93.6	11.1	1207	4	US-10-267-763-8 Sequence 8, Appl
17	61	7.2	780	4	US-09-454-279-17 Sequence 17, Appl
18	60.8	7.2	7218	1	US-08-332-463-14 Sequence 14, Appl
19	59.8	7.1	579	4	US-09-454-279-7 Sequence 7, Appl
20	53.4	6.3	525	4	US-09-454-279-5 Sequence 5, Appl
21	37.6	4.5	4079	4	US-09-016-434-1248 Sequence 1248, Ap
22	37.6	4.5	4517	4	US-09-949-016-4573 Sequence 4573, Ap
23	37.6	4.5	4519	4	US-09-023-655-1202 Sequence 1202, Ap
24	37.6	4.5	4519	4	US-09-949-016-650 Sequence 650, Ap
25	37.6	4.5	4519	4	US-09-492-027-3 Sequence 3, Appl
26	37.2	4.4	1580	4	US-09-252-991A-15307 Sequence 15307, A
27	37.2	4.4	2352	4	US-09-252-991A-15532 Sequence 15532, A

28	37.2	4.4	2916	4	US-09-252-991A-15259 Sequence 15259, A
29	36.8	4.4	2169	3	US-09-434-408-3 Sequence 3, Appl
30	36.6	4.3	5176	3	US-09-610-040-6 Sequence 6, Appl
31	36.6	4.3	5176	4	US-10-267-763-6 Sequence 6, Appl
32	36.4	4.3	601	4	US-09-454-279-3 Sequence 3, Appl
33	35.4	4.2	4403765	3	US-09-103-840A-2 Sequence 2, Appl
34	35.4	4.2	4411529	3	US-09-103-840A-1 Sequence 1, Appl
35	35	4.2	2097	4	US-09-252-991A-13635 Sequence 13635, A
36	35	4.2	2231	4	US-09-252-991A-13809 Sequence 13809, A
37	34.6	4.1	789	4	US-09-252-991A-12701 Sequence 12701, A
38	34.6	4.1	1632	4	US-09-252-991A-13259 Sequence 13259, A
39	34.4	4.1	3008	4	US-09-435-376-6 Sequence 6, Appl
40	34.2	4.1	1509	4	US-09-724-797-89 Sequence 89, Appl
41	34.2	4.1	11958	3	US-09-134-246-8 Sequence 8, Appl
42	34.2	4.1	11958	4	US-09-664-186-8 Sequence 8, Appl
43	34	4.0	705	4	US-09-270-767-5061 Sequence 5061, Ap
44	34	4.0	705	4	US-09-270-767-20343 Sequence 20343, A
45	34	4.0	978	4	US-09-902-540-6442 Sequence 6442, Ap

ALIGNMENTS

RESULT 1  
US-09-248-796A-4110  
Sequence 4110, Application US/09248796A  
Patent No. 6747137

GENERAL INFORMATION:  
APPLICANT: Keith Weinstein et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC

FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 4110

LENGTH: 948  
TYPE: DNA

ORGANISM: Candida albicans  
US-09-248-796A-4110

Query Match  
Best Local Similarity 32.0%; Score 270; DB 4; Length 948;  
Matches 462; Conservative 0; Mismatches 320; Indels 0; Gaps 0;

QY	1	ATGACCTTATGACCAAGAAACAGTGTGACCTTGCAATTAAGAGATGCTTGTC	60
DB	142	ATGATTTTATGAAACCAAACTGCTGATCTTGCAATCCGTAACATCGTAACATTTGTA	201
QY	61	CGATGAGAGATGACATCACTTCACTTATGAGCGGTGCGAGTTCTATCGTCCGC	120
DB	202	AGAGTGAAGATCACTATGTTGTTATTAACGAAAGATTCATTTTCACTGCCCA	261
QY	121	TGGATATCAAGTCAACCAAGTCCCTATTCCTCACTTGAGGCTCGTTGACTG	180
DB	262	TGAGTTATGAAAGATTAATATATATCCCAATTTGATGAACTTTTGGATG	321
QY	181	CTGTTGTCGACAGCAGCAATTCATTCGAGTGAAGATTAACGCGCAGCGAG	240
DB	322	GCTTTGATCAATGGAAGTTCATTCGAAATCAAGCGTTATGAAGACCAAGCA	381
QY	241	GTCCTTTTCCCAAGTGTGCAAAACGTTTGCAGATCACTAACCATG	300
DB	382	ACTCATTTTCCAGATCAATGAAATCCCAATTTTACCCCAATCAATATCTTAA	441
QY	301	GTCGAGGCTCTAGCGGATGAATCAACGTAAGATCTCAAGATCTACAG	360
DB	442	ATATGGCCAAATATTTGATGAAATTAATGTTATTTCTGAATATGAAGTTATGTT	501

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OM nucleic - nucleic search, using SW model

Run on: April 9, 2005, 19:49:03 ; Search time 634 Seconds  
(without alignments)  
8057.702 Million cell updates/sec

Title: US-10-042-059B-1

Perfect score: 843

Sequence: 1 atggacttaccgaagcaga.....tctctctgctgctgactag 843

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5615251 seqs, 303001701 residues 11230502

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
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20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	100.0	843	US-10-042-059A-1	Sequence 1, Appli
2	843	100.0	1655	US-10-042-059A-3	Sequence 3, Appli
3	270	32.0	807	US-10-741-849-6032	Sequence 6032, Ap
4	156.4	18.6	869	US-10-472-587-26	Sequence 26, Appl
5	141.2	16.7	2920	US-10-128-714-249	Sequence 249, App
6	131.4	15.6	1016	US-10-128-714-249	Sequence 5249, A
7	131.4	15.6	1016	US-09-454-279-13	Sequence 93956, A
8	131.4	15.6	1016	US-09-454-279-13	Sequence 13, Appl
9	131.4	15.6	1231	US-10-624-061-13	Sequence 13, Appl
10	118.2	14.0	1423	US-10-424-599-123820	Sequence 123820,
11	116.8	13.9	658	US-10-653-047-6992	Sequence 6992, Ap

12	116.6	13.8	1146	17	US-10-425-114-7285	Sequence 7285, Ap
13	116	13.8	1376	18 <td>US-10-425-115-102347</td> <td>Sequence 102347,</td>	US-10-425-115-102347	Sequence 102347,
14	112.2	13.3	1548	18 <td>US-10-739-930-4455</td> <td>Sequence 4455, Ap</td>	US-10-739-930-4455	Sequence 4455, Ap
15	111.2	13.2	1223	9 <td>US-09-454-279-11</td> <td>Sequence 11, Appl</td>	US-09-454-279-11	Sequence 11, Appl
16	111.2	13.2	1223	17 <td>US-10-624-061-11</td> <td>Sequence 11, Appl</td>	US-10-624-061-11	Sequence 11, Appl
17	111.2	13.2	1500	18 <td>US-10-767-701-14353</td> <td>Sequence 14353, A</td>	US-10-767-701-14353	Sequence 14353, A
18	110.6	13.1	1010	18 <td>US-10-425-115-102351</td> <td>Sequence 102351,</td>	US-10-425-115-102351	Sequence 102351,
19	109.6	13.0	1397	18 <td>US-10-425-115-102346</td> <td>Sequence 102346,</td>	US-10-425-115-102346	Sequence 102346,
20	104.4	12.4	1217	14 <td>US-10-267-763-4</td> <td>Sequence 4, Appli</td>	US-10-267-763-4	Sequence 4, Appli
21	104.4	12.4	1217	14 <td>US-10-267-763-10</td> <td>Sequence 10, Appl</td>	US-10-267-763-10	Sequence 10, Appl
22	103.2	12.2	1368	18 <td>US-10-425-115-102349</td> <td>Sequence 102349,</td>	US-10-425-115-102349	Sequence 102349,
23	99.8	11.8	1020	9 <td>US-09-454-279-15</td> <td>Sequence 15, Appli</td>	US-09-454-279-15	Sequence 15, Appli
24	99.8	11.8	1020	17 <td>US-10-624-061-15</td> <td>Sequence 15, Appli</td>	US-10-624-061-15	Sequence 15, Appli
25	99.8	11.8	1079	17 <td>US-10-425-114-7639</td> <td>Sequence 7639, Ap</td>	US-10-425-114-7639	Sequence 7639, Ap
26	97.4	11.6	798	9 <td>US-09-938-842A-972</td> <td>Sequence 972, App</td>	US-09-938-842A-972	Sequence 972, App
27	97.4	11.6	798	11 <td>US-09-938-842A-972</td> <td>Sequence 972, App</td>	US-09-938-842A-972	Sequence 972, App
28	97.4	11.6	1006	14 <td>US-10-267-763-3</td> <td>Sequence 3, Appli</td>	US-10-267-763-3	Sequence 3, Appli
29	97.4	11.6	1006	14 <td>US-10-267-763-9</td> <td>Sequence 9, Appli</td>	US-10-267-763-9	Sequence 9, Appli
30	97	11.5	1430	18 <td>US-10-739-930-4454</td> <td>Sequence 4454, Ap</td>	US-10-739-930-4454	Sequence 4454, Ap
31	93.6	11.1	1005	9 <td>US-09-938-842A-737</td> <td>Sequence 737, App</td>	US-09-938-842A-737	Sequence 737, App
32	93.6	11.1	1005	11 <td>US-09-938-842A-737</td> <td>Sequence 737, App</td>	US-09-938-842A-737	Sequence 737, App
33	93.6	11.1	1207	14 <td>US-10-267-763-2</td> <td>Sequence 2, Appli</td>	US-10-267-763-2	Sequence 2, Appli
34	93.6	11.1	1207	14 <td>US-10-267-763-8</td> <td>Sequence 8, Appli</td>	US-10-267-763-8	Sequence 8, Appli
35	93.6	11.1	1299	18 <td>US-10-739-930-621</td> <td>Sequence 621, App</td>	US-10-739-930-621	Sequence 621, App
36	87.6	10.4	1653	17 <td>US-10-424-599-93036</td> <td>Sequence 93036, A</td>	US-10-424-599-93036	Sequence 93036, A
37	81	9.6	880	17 <td>US-10-425-114-3898</td> <td>Sequence 3898, Ap</td>	US-10-425-114-3898	Sequence 3898, Ap
38	80	9.5	1314	18 <td>US-10-425-115-151470</td> <td>Sequence 151470,</td>	US-10-425-115-151470	Sequence 151470,
39	78.4	9.3	1197	17 <td>US-10-425-114-27576</td> <td>Sequence 27576, A</td>	US-10-425-114-27576	Sequence 27576, A
40	77.2	9.2	524	18 <td>US-10-425-115-102342</td> <td>Sequence 102342,</td>	US-10-425-115-102342	Sequence 102342,
41	76.2	9.0	768	18 <td>US-10-437-963-49372</td> <td>Sequence 49372, A</td>	US-10-437-963-49372	Sequence 49372, A
42	74.8	8.9	2154	18 <td>US-10-437-963-83557</td> <td>Sequence 83557, A</td>	US-10-437-963-83557	Sequence 83557, A
43	74.2	8.8	1066	17 <td>US-10-425-114-13332</td> <td>Sequence 13332, Ap</td>	US-10-425-114-13332	Sequence 13332, Ap
44	74.2	8.8	1083	18 <td>US-10-425-115-115559</td> <td>Sequence 115559,</td>	US-10-425-115-115559	Sequence 115559,
45	73	8.7	580	18 <td>US-10-021-923-12291</td> <td>Sequence 12291, A</td>	US-10-021-923-12291	Sequence 12291, A

#### ALIGNMENTS

RESULT 1  
US-10-042-059A-1  
Sequence 1, Application US/10042059A  
Publication No. US20020197704A1  
GENERAL INFORMATION:  
APPLICANT: Rhein Biotech Gesellschaft fur neue biotechnologische Prozesse und  
APPLICANT: Producte mbH  
TITLE OF INVENTION: Nucleic Acid Molecule Containing a Nucleic Acid Coding for a Pol  
FILE REFERENCE: PA30588US-019  
CURRENT FILING DATE: 2001-10-25  
PRIOR APPLICATION NUMBER: DE 199 19 124.7  
PRIOR FILING DATE: 1999-04-27  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 1  
LENGTH: 843  
TYPE: DNA  
ORGANISM: Haemulula polymorpha  
US-10-042-059A-1

Query Match 100.0%; Score 843; DB 13; Length 843;  
Best Local Similarity 100.0%; Pred. No. 6,4e-267;  
Matches 843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTTTATGAAAGCAAGAGTGTGACCTTGCAACATTAGAGATGCTGTC 60  
DB 1 ATGACTTTATGAAAGCAAGAGTGTGACCTTGCAACATTAGAGATGCTGTC 60  
QY 61 CGATGAGGATGATGATCATCTTCACTTTATGAGGGGTGAGATTATGCGTGGCC 120  
DB 61 CGATGAGGATGATGATCATCTTCACTTTATGAGGGGTGAGATTATGCGTGGCC 120

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 19:31:58 ; Search time 3556 Seconds

(without alignments)  
9023.672 Million cell updates/sec

Title: US-10-042-059b-1

Perfect score: 843  
Sequence: 1 atgagactatgaagccagca.....tctctctgctgtctag 843

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_esc1:\*  
2: gb\_esc2:\*  
3: gb\_esc3:\*  
4: gb\_esc4:\*  
5: gb\_esc5:\*  
6: gb\_esc6:\*  
7: gb\_esc7:\*  
8: gb\_esc8:\*  
9: gb\_esc9:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	299	35.5	1185	CNS06T5P	AL414131 T7 end of
2	176.6	20.9	937	CNS06T5P	AL415049 T3 end of
3	176.6	20.9	1052	CNS06T5P	AL419633 T3 end of
4	140	16.6	948	CNS06T5P	CO005472 EST793807
5	137	16.3	574	BZ303243	BZ303243 KD2284.D1
6	132.8	15.8	738	CF877247	CF877247 cric075xb
7	132.8	15.8	816	CB905545	CB905545 tric075xb
8	125.4	14.9	788	CO165801	CO165801 PBD1_57_F
9	121.6	14.4	660	BX253798	BX253798 BX253798
10	116.8	13.9	798	CB619881	CB619881 OS118a04L
11	116.2	13.8	652	CD423256	CD423256 SA1_28_B1
12	113.8	13.5	747	CNS06T5P	AL415049 T3 end of
13	113.2	13.4	710	CF475712	CF475712 RTW2_11_
14	111.2	13.2	1222	AY103806	AY103806 Zea mays
15	107.4	12.7	827	CO162312	CO162312 PBD1_34_B
16	106	12.6	988	AJ833468	AJ833468 AJ833468
17	105.8	12.6	602	CD982471	CD982471 QAK5C04.x
18	105.8	12.6	903	CN149106	CN149106 MOUNDI_60
19	105.6	12.5	527	CO165812	CO165812 PBD1_57_F
20	104.6	12.4	606	BI995968	BI995968 1031032C0
21	103	12.2	737	CO005473	CO005473 EST793808
22	103	12.2	867	CB619882	CB619882 OS118a04L
23	102.8	12.2	727	CA121888	CA121888 SCUPR105
24	102.2	12.1	680	CA080410	CA080410 SCVPM105

25	100.8	12.0	551	5	BQ701847	BQ701847 NX51_121
26	99.4	11.8	605	7	CN913779	CN913779 030108ABM
27	98.6	11.7	607	8	BZ296833	BZ296833 CG3070..r1
28	98	11.6	495	1	AA786587	AA786587 m5b08a1.f
29	97.8	11.6	821	7	CK196570	CK196570 FGAS00523
30	97.4	11.6	837	7	CO366854	CO366854 RTK1_30_C
31	97	11.5	596	8	BZ298767	BZ298767 CG4569..r1
32	97	11.5	781	7	CF667838	CF667838 RTK1_32
33	96.6	11.5	853	7	CO366784	CO366784 RTK1_30_C
34	96.2	11.4	657	9	AG273371	AG273371 Cyanidios
35	96	11.4	812	7	CN148636	CN148636 MOUNDI_57
36	95	11.3	885	7	CV274873	CV274873 WS0174..B2
37	94.8	11.2	857	7	CF635400	CF635400 zmrw00..r1
38	94.6	11.2	480	7	CV002646	CV002646 na003-13c
39	94.4	11.2	707	6	CA239381	CA239381 SCREFL503
40	94.2	11.2	785	7	CNS23137	CNS23137 G0015M01.
41	93.6	11.1	552	4	B1718858	B1718858 1031032C0
42	93.6	11.1	1265	3	CNS046WL	BX824460 Arabidops
43	93.6	11.1	1329	3	CNS0A727	BX822129 Arabidops
44	93.2	11.1	698	2	BE577489	BE577489 L48-2335T
45	93.2	11.1	830	6	CB622596	CB622596 OS118a091

## ALIGNMENTS

RESULT 1	CNS06T5P	1185 bp	DNA	linear	GSS 05-JUL-2001
LOCUS	CNS06T5P	T7 end of clone AW0AA029A11 of library AW0AA from strain CL18 89 of			
DEFINITION	Yarrowia lipolytica, genomic survey sequence.				
ACCESSION	AL414131.1	GI:12186949			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Yarrowia lipolytica				
REFERENCE	Yarrowia lipolytica				
AUTHORS	Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia.				
	1 (bases 1 to 1185)				
	Soucier, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolochin-Fukuhara, M., Bon, E., Broctier, P., Casaregola, S., de-Montigny, J., Dujon, B., Duren, P., Lepingle, A., Liorette, B., Malpertuy, A., Neveuglise, C., Ozier-Kalogeropoulos, O., Pottier, S., Saurin, M., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.				
	Genomic exploration of the hemiascomycete yeasts: 1. A set of yeast species for molecular evolution studies				
	FBS Lett. 487 (1), 3-12 (2000)				
	1152876				
	2 (bases 1 to 1185)				
	Casaregola, S., Neveuglise, C., Lepingle, A., Bon, E., Feynerol, C., Artiguenave, F., Wincker, P. and Gaillardin, C.				
	Genomic exploration of the hemiascomycete yeasts: 17. Yarrowia lipolytica				
	FBS Lett. 487 (1), 95-100 (2000)				
	1152882				
	3 (bases 1 to 1185)				
	Direct Submission				
	Genoscope.				
	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Crémieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail: seqrefgenoscope.cns.fr - Web: www.genoscope.cns.fr)				
	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces kluyveri, Saccharomyces servazii, Zygosaccharomyces rouxi, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angustis, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of				

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 21:57:48 / Search time 416 Seconds  
(without alignments)  
9924.137 Million cell updates/sec

Title: US-10-042-059b-1

Perfect score: 843  
Sequence: 1 atgagcttcatgagcaga.....ctctctcgtctgtagag 843

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pal:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	100.0	843	6	BD266599 Nucleic a
2	843	100.0	843	6	AX043758 Sequence
3	843	100.0	1652	8	AF204738 Pictha an
4	843	100.0	1655	6	BD266600 Nucleic a
5	843	100.0	1655	6	AX043760 Sequence
6	22	2.6	1029	9	GM012286 U12286 Glycine max
7	21	2.5	109431	9	AC016696 AC016696 Homo sapi
8	21	2.5	127532	10	AC117812 AC117812 Mus muscu
9	21	2.5	161517	9	AC009520 AC009520 Homo sapi
10	21	2.5	163194	3	LMPP214 AL449144 Leishmani
11	21	2.5	176202	2	AC022369 AC022369 Mus muscu
12	21	2.5	180210	2	AC109156 Mus muscu
13	21	2.5	278353	2	AC106122 Rattus no
14	20	2.4	529	9	HS43161 Homo sapi
15	20	2.4	731	8	ATH523052 Arabidops
16	20	2.4	1185	8	BD179999 Arabidops
17	20	2.4	1205	8	AF462807 Arabidops
18	20	2.4	1283	8	AY086467 Arabidops
19	20	2.4	1425	10	AF295369 Mus muscu

20	2.4	1493	10	AF165986 AF165986 Mus muscu
21	2.4	2250	8	ATU09376 ATU09376 Mus muscu
22	2.4	2479	6	BC029750 BC029750 Mus muscu
23	2.4	3873	9	CQ849743 CQ849743 Sequence
24	2.4	3873	9	AX126783 Homo sapi
25	2.4	4149	9	BC041850 Homo sapi
26	2.4	4322	8	AF486633 Arabidops
27	2.4	10737	1	AE013312 AE013312 Methanosa
28	2.4	11287	1	AE011116 AE011116 Methanosa
29	2.4	38435	6	AC106801 AC106801 Homo sapi
30	2.4	95769	6	AX652128 AX652128 Sequence
31	2.4	95769	2	AC013430 AC013430 Genomic s
32	2.4	110000	8	AF006501 AF006501 Continuation (2 of
33	2.4	110000	8	CR382132 CR382132 Continuation (36 o
34	2.4	110000	8	AE016817 AE016817_12
35	2.4	118466	6	CQ870115 CQ870115 Sequence
36	2.4	124409	9	AC069360 AC069360 Homo sapi
37	2.4	131703	2	AC104642 AC104642 Trypanoso
38	2.4	150054	9	AL161901 AL161901 Human DNA
39	2.4	152593	8	AC002332 AC002332 Arabidops
40	2.4	154814	9	AC114802 AC114802 Homo sapi
41	2.4	156556	2	AC151236 AC151236 Bos tauru
42	2.4	167385	2	CR753906 CR753906 Dantio rer
43	2.4	176580	10	AC127265 AC127265 Mus muscu
44	2.4	177623	10	AC138667 AC138667 Mus muscu
45	2.4	182032	2	AC150435 AC150435 Atelesrix
46	2.4	188006	2	AC147422 AC147422 Oryctolag
47	2.4	192634	2	AC069466 AC069466 Mus muscu
48	2.4	193614	10	AC110219 AC110219 Mus muscu
49	2.4	194045	10	AL833774 AL833774 Mouse DNA
50	2.4	208065	9	AC008676 AC008676 Homo sapi
51	2.4	209945	2	AC139756 AC139756 Mus muscu
52	2.4	210025	2	CR376847 CR376847 Dantio rer
53	2.4	221610	2	AC134861 AC134861 Mus muscu
54	2.4	237933	2	AC111638 AC111638 Rattus no
55	2.4	239343	2	AC106481 AC106481 Rattus no
56	2.4	253961	2	AC128235 AC128235 Rattus no
57	2.4	254581	2	AC111674 AC111674 Rattus no
58	2.4	257570	2	CR354431 CR354431 Dantio rer
59	2.4	257676	10	AL844852 AL844852 Mouse DNA
60	2.4	260692	2	AC134896 AC134896 Mus muscu
61	2.4	261934	5	BX664745 BX664745 Zebrafish
62	2.4	274676	1	AE017305 AE017305 Thermus t
63	2.4	295971	2	AC096027 AC096027 Rattus no
64	2.4	348672	1	CR378670 CR378670 Photobact
65	2.3	28	6	BD266604 BD266604 Nucleic a
66	2.3	51	6	CQ001947 CQ001947 Sequence
67	2.3	51	6	CQ002131 CQ002131 Sequence
68	2.3	243	4	PCMYO18 AF008572 Felis cat
69	2.3	261	4	RABMYV82 K01697 Rabbit vent
70	2.3	344	6	RABMYV82 K01696 Rabbit vent
71	2.3	344	6	AX462426 AX462426 Sequence
72	2.3	471	6	AX331324 AX331324 Sequence
73	2.3	471	6	AX331324 AX331324 Sequence
74	2.3	483	6	AX778298 AX778298 Sequence
75	2.3	575	10	OCOTARP MS7669 Octodon deg
76	2.3	687	6	AR491514 AR491514 Sequence
77	2.3	687	6	AR491514 AR491514 Sequence
78	2.3	702	4	S62056 S62056 myosin alph
79	2.3	751	11	BV041536 BV041536 Homo sapi
80	2.3	775	9	HS432530 HS432530 Homo sapi
81	2.3	870	6	BD211751 BD211751 Proteins
82	2.3	954	8	AF026397 AF026397 Homo sapi
83	2.3	1145	8	AK110798 AK110798 Oryza sat
84	2.3	1166	9	BC007918 BC007918 Homo sapi
85	2.3	1176	3	BT011191 BT011191 Drosophi
86	2.3	1214	6	AR491513 AR491513 Sequence
87	2.3	1214	6	AX214360 AX214360 Sequence
88	2.3	1394	4	RABMYV82 K02443 Rabbit card
89	2.3	1514	4	HSU47925 U47925 Human prote
90	2.3	1515	6	CQ722412 CQ722412 Sequence
91	2.3	1544	9	BC080585 BC080585 Homo sapi
92	2.3	1638	9	BC002353 BC002353 Homo sapi



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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 19:59:02 ; Search time 586 Seconds  
(without alignments)  
8515.942 Million cell updates/sec

Title: US-10-042-059B-1

Perfect score: 843  
Sequence: 1 atcgacttatgaagcaga.....tctctctgctgctgtag 843

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 100 summaries

Database :

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1: geneeqn1980s:\*  
2: geneeqn1990s:\*  
3: geneeqn2000s:\*  
4: geneeqn2001as:\*  
5: geneeqn2001bs:\*  
6: geneeqn2002as:\*  
7: geneeqn2002bs:\*  
8: geneeqn2003as:\*  
9: geneeqn2003bs:\*  
10: geneeqn2003cs:\*  
11: geneeqn2003ds:\*  
12: geneeqn2004as:\*  
13: geneeqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	100.0	843	3 AAC81949	AAC81949 H. polymo
2	843	100.0	1655	3 AAC81950	AAC81950 H. polymo
3	20	2.4	484	3 AAC37122	AAC37122 Arabidops
4	20	2.4	1044	13 ADS59363	ADS59363 Bacteri
5	20	2.4	1283	3 AAC47972	AAC47972 Arabidops
6	20	2.4	3873	13 ADRO6706	ADRO6706 Full leng
7	20	2.4	95769	8 ADA86859	ADA86859 Arabidops
8	20	2.4	118466	13 ABD32861	ABD32861 Human can
9	19	2.3	28	4 AAC81954	AAC81954 H. polymo
10	19	2.3	51	4 AAL27379	AAL27379 Human SNP
11	19	2.3	51	4 AAL27379	AAL27379 Human SNP
12	19	2.3	334	12 ADJ40487	ADJ40487 Plant CDN
13	19	2.3	344	6 ABQ92902	ABQ92902 Tyriticum
14	19	2.3	369	6 AAL85587	AAL85587 Human pol
15	19	2.3	471	6 ABL63496	ABL63496 Breast ca
16	19	2.3	483	10 ADF79899	ADF79899 Leukaemia
17	19	2.3	507	13 ACN61244	ACN61244 Cotton gy
18	19	2.3	507	13 ADP29185	ADP29185 Human sec
19	19	2.3	555	12 AAF80049	AAF80049 Human sec
20	19	2.3	565	13 ACN53545	ACN53545 Cotton an

21	19	2.3	589	12 ADL86198	ADL86198 DNA up-re
22	19	2.3	589	12 ADL86199	ADL86199 DNA up-re
23	19	2.3	676	12 ADJ42606	ADJ42606 Plant CDN
24	19	2.3	870	3 AAZ57841	AAZ57841 Protein r
25	19	2.3	1214	5 AAS11360	AAS11360 Rice DNA
26	19	2.3	1514	13 ADR25630	ADR25630 Breast ca
27	19	2.3	1629	10 ADP70560	ADP70560 Orphan re
28	19	2.3	1767	12 ADO29954	ADO29954 Human GPC
29	19	2.3	1931	4 ABH06323	ABH06323 Drosophi
30	19	2.3	1980	13 ADS49231	ADS49231 Bacteri
31	19	2.3	2516	8 ABZ42526	ABZ42526 Human pro
32	19	2.3	2516	13 ADQ085304	ADQ085304 Human tum
33	19	2.3	2516	13 ADR25958	ADR25958 Breast ca
34	19	2.3	2890	13 ADM85116	ADM85116 Mouse ato
35	19	2.3	3219	11 ADM02536	ADM02536 Human CDN
36	19	2.3	3331	4 ABH06322	ABH06322 Drosophi
37	19	2.3	5661	2 AAV21518	AAV21518 Rattus no
38	19	2.3	5886	13 ADS97707	ADS97707 Rattus al
39	19	2.3	5918	11 ACN924725	ACN924725 Breast ca
40	19	2.3	5925	12 ADP72935	ADP72935 Renal tox
41	19	2.3	5930	10 ADS52833	ADS52833 Primary r
42	19	2.3	12801	13 ADS97709	ADS97709 Rattus al
43	19	2.3	222930	6 ABR84349	ABR84349 Human CDN
44	18	2.1	309	6 ACI61334	ACI61334 Human m/c
45	18	2.1	333	5 AAF80051	AAF80051 Nucleotid
46	18	2.1	369	12 ADP93391	ADP93391 Cotton ex
47	18	2.1	405	9 ACH49258	ACH49258 Human leu
48	18	2.1	408	5 AAF80053	AAF80053 Nucleotid
49	18	2.1	537	13 ADR61828	ADR61828 Cotton CD
50	18	2.1	580	12 ACH69149	ACH69149 Human gen
51	18	2.1	586	13 ACN58170	ACN58170 Cotton gy
52	18	2.1	592	13 ADQ054235	ADQ054235 Novel can
53	18	2.1	732	5 AAS6702	AAS6702 DNA encod
54	18	2.1	741	12 ADI45730	ADI45730 Corn leop
55	18	2.1	741	12 ADJ44921	ADJ44921 Plant CDN
56	18	2.1	786	4 AAL02364	AAL02364 Human rep
57	18	2.1	804	13 ADS49193	ADS49193 Bacteri
58	18	2.1	808	5 AAF80052	AAF80052 Nucleotid
59	18	2.1	819	2 AAX99545	AAX99545 Nucleic a
60	18	2.1	897	5 AAF80050	AAF80050 Nucleotid
61	18	2.1	939	10 ADK54895	ADK54895 Plant DNA
62	18	2.1	954	13 ADS48734	ADS48734 Bacteri
63	18	2.1	1231	4 AAH34429	AAH34429 Human col
64	18	2.1	1434	3 AAC59740	AAC59740 Human sec
65	18	2.1	1434	8 ABZ73345	ABZ73345 Secreted
66	18	2.1	1434	8 ADA97947	ADA97947 Human sec
67	18	2.1	1434	8 ADA43853	ADA43853 Human sec
68	18	2.1	1434	10 ADC20102	ADC20102 Human sec
69	18	2.1	1434	10 ADP10566	ADP10566 Human sec
70	18	2.1	1434	10 ABZ66953	ABZ66953 Human sec
71	18	2.1	1458	4 AAC84376	AAC84376 Mouse CRD
72	18	2.1	1480	6 ABL39716	ABL39716 Human NS
73	18	2.1	1501	2 AAT09257	AAT09257 Human ara
74	18	2.1	1696	12 ADM47884	ADM47884 Polynucle
75	18	2.1	1904	12 ADQ63411	ADQ63411 Novel hum
76	18	2.1	1967	13 ADQ68139	ADQ68139 Human tum
77	18	2.1	2019	10 ADB62069	ADB62069 Human tum
78	18	2.1	2020	6 AAS94898	AAS94898 Human DNA
79	18	2.1	2056	11 ACN90880	ACN90880 Breast ca
80	18	2.1	2088	13 ACN10128	ACN10128 Human the
81	18	2.1	2097	2 AAV26543	AAV26543 Human ret
82	18	2.1	2115	3 AAT96642	AAT96642 Human TUL
83	18	2.1	2115	3 AAB94635	AAB94635 Human TUL
84	18	2.1	2163	6 AEN96944	AEN96944 Gene #344
85	18	2.1	2163	9 ADB11525	ADB11525 Allicococ
86	18	2.1	2278	9 ACA98960	ACA98960 CDNA enco
87	18	2.1	2400	13 ADRO6553	ADRO6553 Full leng
88	18	2.1	2420	4 ABL17625	ABL17625 Drosophi
89	18	2.1	2484	4 ABL03465	ABL03465 Drosophi
90	18	2.1	2540	5 AAF80049	AAF80049 Nucleotid
91	18	2.1	2856	5 AAF80048	AAF80048 Nucleotid
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 22:08:23 / Search time 194 Seconds  
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7110.213 Million cell updates/sec

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	20	2.4	98862	4 US-09-949-016-14133	Sequence 14133, A
2	20	2.4	102884	4 US-09-949-016-17100	Sequence 17100, A
3	19	2.3	687	4 US-09-780-717-30	Sequence 30, Appl
4	19	2.3	1214	4 US-09-780-717-28	Sequence 28, Appl
5	19	2.3	5661	3 US-08-938-105-2	Sequence 2, Appl
6	19	2.3	89210	4 US-09-949-016-16988	Sequence 16988, A
7	18	2.1	333	4 US-09-684-708A-8	Sequence 8, Appl
8	18	2.1	408	4 US-09-684-708A-12	Sequence 12, Appl
9	18	2.1	601	4 US-09-949-016-22999	Sequence 22999, A
10	18	2.1	601	4 US-09-949-016-23000	Sequence 23000, A
11	18	2.1	601	4 US-09-949-016-41205	Sequence 41205, A
12	18	2.1	601	4 US-09-949-016-41206	Sequence 41206, A
13	18	2.1	808	4 US-09-684-708A-10	Sequence 10, Appl
14	18	2.1	819	4 US-09-601-198-45	Sequence 45, Appl
15	18	2.1	819	4 US-09-270-767-10691	Sequence 10691, A
16	18	2.1	897	4 US-09-684-708A-6	Sequence 6, Appl
17	18	2.1	1581	4 US-09-949-016-243	Sequence 243, Appl
18	18	2.1	1588	4 US-09-949-016-1165	Sequence 1165, Ap
19	18	2.1	2115	3 US-09-032-365A-12	Sequence 12, Appl
20	18	2.1	2116	1 US-08-701-380-1	Sequence 1, Appl
21	18	2.1	2184	3 US-08-955-918C-1	Sequence 1, Appl
22	18	2.1	2184	3 US-08-697-766A-1	Sequence 1, Appl
23	18	2.1	2540	4 US-09-684-708A-4	Sequence 4, Appl
24	18	2.1	2856	4 US-09-684-708A-1	Sequence 1, Appl
25	18	2.1	8438	1 US-07-945-283-1	Sequence 1, Appl
26	18	2.1	8590	1 US-09-949-016-5562	Sequence 5562, Ap
27	18	2.1	10300	4 US-09-949-016-636	Sequence 636, Ap

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35	18	2.1	57280	4 US-09-949-016-12846	Sequence 12846, A
36	18	2.1	57280	4 US-09-949-016-13542	Sequence 13542, A
37	18	2.1	57280	4 US-09-949-016-13543	Sequence 13543, A
38	18	2.1	57280	4 US-09-949-016-13544	Sequence 13544, A
39	18	2.1	57280	4 US-09-949-016-13545	Sequence 13545, A
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50	18	2.1	288031	4 US-09-949-016-14864	Sequence 14864, A
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52	18	2.1	4411529	3 US-09-103-840A-2	Sequence 1, Appl
53	17	2.0	278	4 US-09-640-211A-1368	Sequence 1368, Ap
54	17	2.0	288	4 US-09-252-991A-1801	Sequence 1801, Ap
55	17	2.0	562	4 US-09-663-751-224	Sequence 224, Appl
56	17	2.0	601	4 US-09-949-016-134896	Sequence 134896, A
57	17	2.0	601	4 US-09-949-016-134897	Sequence 134897, A
58	17	2.0	747	4 US-09-949-016-188364	Sequence 188364, A
59	17	2.0	747	3 US-08-750-145A-19	Sequence 19, Appl
60	17	2.0	747	3 US-08-975-698A-23	Sequence 23, Appl
61	17	2.0	747	3 US-09-417-090-23	Sequence 23, Appl
62	17	2.0	747	3 US-09-727-578-23	Sequence 23, Appl
63	17	2.0	940	2 US-08-713-000-3	Sequence 3, Appl
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68	17	2.0	1048	4 US-09-270-767-11465	Sequence 11465, A
69	17	2.0	1062	4 US-09-252-991A-3271	Sequence 3271, Ap
70	17	2.0	1098	4 US-09-902-540-3112	Sequence 3112, Ap
71	17	2.0	1144	4 US-09-640-211A-154	Sequence 154, Ap
72	17	2.0	1169	4 US-09-596-002-2	Sequence 2, Appl
73	17	2.0	1305	4 US-09-902-540-4277	Sequence 4277, Ap
74	17	2.0	1440	4 US-09-023-655-1399	Sequence 1399, Ap
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85	17	2.0	4251	4 US-09-902-540-536	Sequence 536, Ap
86	17	2.0	4692	2 US-08-916-917-1	Sequence 1, Appl
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90	17	2.0	4692	2 US-08-672-211-1	Sequence 1, Appl
91	17	2.0	4692	3 US-09-225-170-1	Sequence 1, Appl
92	17	2.0	7014	4 US-09-949-016-15169	Sequence 15169, A
93	17	2.0	18809	4 US-09-902-540-1141	Sequence 1141, Ap
94	17	2.0	22294	4 US-09-949-016-15522	Sequence 15522, A
95	17	2.0	26012	4 US-09-902-540-1212	Sequence 1212, Ap
96	17	2.0	27630	4 US-09-949-016-12722	Sequence 12722, A
97	17	2.0	32207	2 US-08-770-379-20	Sequence 20, Appl
98	17	2.0	32207	3 US-08-757-669A-20	Sequence 20, Appl
99	17	2.0	32207	3 US-09-230-371A-20	Sequence 20, Appl
100	17	2.0	36138	4 US-08-311-731A-136	Sequence 136, Appl

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	843	100.0	1655	US-10-047-059A-3	Sequence 3, Appli
3	22	2.6	1936	US-10-424-589-58517	Sequence 35817, A
4	20	2.4	1044	US-10-368-493-35037	Sequence 35037, A
5	20	2.4	1309	US-10-425-114-23242	Sequence 23242, A
6	19	2.3	334	US-10-260-238-1487	Sequence 1487, Ap
7	19	2.3	471	US-09-954-531-766	Sequence 766, App
8	19	2.3	471	US-09-954-531-1201	Sequence 1201, Ap
9	19	2.3	471	US-10-843-641A-1833	Sequence 1833, Ap
10	19	2.3	471	US-10-843-641A-2268	Sequence 2268, Ap
11	19	2.3	507	US-10-021-333-16025	Sequence 16025, A

12	19	2.3	565	US-10-021-323-8326	Sequence 8326, Ap
13	19	2.3	589	US-10-430-201-2591	Sequence 2591, Ap
14	19	2.3	589	US-10-430-201-2592	Sequence 2592, Ap
15	19	2.3	676	US-10-260-238-3606	Sequence 3606, Ap
16	19	2.3	687	US-09-780-717-30	Sequence 30, Appli
17	19	2.3	1214	US-09-780-717-28	Sequence 28, Appli
18	19	2.3	1514	US-10-172-118-1491	Sequence 1491, Ap
19	19	2.3	1514	US-10-347-887-1491	Sequence 1491, Ap
20	19	2.3	1786	US-10-738-930-5058	Sequence 5058, Ap
21	19	2.3	1980	US-10-369-433-27661	Sequence 27661, A
22	19	2.3	2069	US-10-437-963-32618	Sequence 32618, A
23	19	2.3	2516	US-10-225-567A-533	Sequence 533, App
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28	19	2.3	5918	US-10-198-846-13875	Sequence 13875, A
29	19	2.3	5925	US-10-191-803-104	Sequence 104, App
30	19	2.3	12801	US-10-798-037-5	Sequence 5, Appli
31	19	2.3	23810	US-10-741-600-17925	Sequence 17925, A
32	18	2.1	25	US-10-098-263B-61335	Sequence 61335, A
33	18	2.1	231	US-10-242-555A-4564	Sequence 4564, Ap
34	18	2.1	231	US-10-085-783A-4564	Sequence 4564, Ap
35	18	2.1	247	US-10-425-115-24483	Sequence 94483, A
36	18	2.1	315	US-10-437-963-10812	Sequence 10812, A
37	18	2.1	337	US-10-425-114-22093	Sequence 22093, A
38	18	2.1	360	US-10-425-115-171112	Sequence 171112, A
39	18	2.1	369	US-09-732-627A-2402	Sequence 2402, Ap
40	18	2.1	405	US-09-918-995-36470	Sequence 36470, A
41	18	2.1	432	US-10-437-963-39613	Sequence 39613, A
42	18	2.1	471	US-10-437-963-16623	Sequence 16623, A
43	18	2.1	505	US-10-425-115-83642	Sequence 93642, A
44	18	2.1	537	US-10-757-795-2609	Sequence 2609, Ap
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47	18	2.1	599	US-10-767-701-24405	Sequence 24405, A
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58	18	2.1	822	US-10-156-761-344	Sequence 344, App
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67	18	2.1	1683	US-10-424-599-13751	Sequence 13751, A
68	18	2.1	1689	US-10-425-115-55404	Sequence 55404, A
69	18	2.1	1696	US-10-310-154-302	Sequence 302, App
70	18	2.1	1774	US-10-437-963-94064	Sequence 94064, A
71	18	2.1	1952	US-10-767-701-12942	Sequence 12942, A
72	18	2.1	2019	US-10-104-047-223	Sequence 223, App
73	18	2.1	2020	US-10-240-965-153	Sequence 153, App
74	18	2.1	2056	US-10-198-846-12030	Sequence 12030, A
75	18	2.1	2116	US-09-880-107-3441	Sequence 3441, Ap
76	18	2.1	2145	US-10-437-963-40675	Sequence 40675, A
77	18	2.1	2417	US-10-437-963-40678	Sequence 40678, A
78	18	2.1	2745	US-10-027-632-112242	Sequence 112242, A
79	18	2.1	2745	US-10-027-632-112242	Sequence 112242, A
80	18	2.1	2912	US-10-437-963-68337	Sequence 68337, A
81	18	2.1	3190	US-10-108-260A-2339	Sequence 2339, Ap
82	18	2.1	4370	US-09-764-891-9644	Sequence 9644, Ap
83	18	2.1	6822	US-10-425-115-129369	Sequence 129369, A
84	18	2.1	10300	US-09-960-253-145	Sequence 145, App

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 20:58:23 / Search time 3558 Seconds  
(without alignments)  
9018.600 Million cell updates/sec

Title: US-10-042-059b-1

Perfect score: 843

Sequence: 1 atgagcttattgaagcagca.....tctctctcgtctgactag 843

Scoring table: OLIGO\_NUC  
Gapop\_60.0, Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database: EST:

1: gb\_esc1:\*  
2: gb\_esc2:\*  
3: gb\_esc3:\*  
4: gb\_esc4:\*  
5: gb\_esc5:\*  
6: gb\_esc6:\*  
7: gb\_esc7:\*  
8: gb\_esc8:\*  
9: gb\_esc9:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2.8	567	6	CB456917	CB456917 714231 MA
2	2.7	615	7	CO889914	CO889914 Bovgen.18
3	2.7	781	5	BX881595	BX881595 EX881595
4	2.6	246	2	AW705733	AW705733 BK51B05.Y
5	2.6	279	7	CK124266	CK124266 BES182410
6	2.6	319	1	AI959790	AI959790 sc94b09.Y
7	2.6	443	4	BM309799	BM309799 bak66g05.
8	2.6	573	6	CD402848	CD402848 Gm CK2544
9	2.6	601	2	BP258490	BP258490 HVSMEF001
10	2.6	626	2	BE661641	BE661641 2-G11 Gma
11	2.6	657	4	BI958372	BI958372 HVSMEH001
12	2.6	662	2	AW349601	AW349601 GM210005A
13	2.6	1093	9	CNS07768	AL432294 T7 end of
14	2.5	63	9	CR068930	Forward s
15	2.5	233	2	BP911142	BP911142 PML-UT006
16	2.5	247	2	BP909761	BP909761 PML-UT006
17	2.5	263	2	BP910260	BP910260 PML-UT006
18	2.5	263	2	AW477877	AW477877 17402 MAR
19	2.5	441	6	CB931218	CB931218 r154b09.Y
20	2.5	488	8	BZ302958	BZ302958 KD2125.G1
21	2.5	496	2	BP074380	BP074380 221782 MA
22	2.5	496	6	CB455541	CB455541 712687 MA
23	2.5	540	2	BE012467	BE012467 121924 MA
24	2.5	549	4	BI359976	BI359976 384767 MA

25	2.5	563	5	BQ119118	BQ119118 EST604694
26	2.5	593	7	BK665191	BK665191 BX665191
27	2.5	593	7	CK838080	CK838080 4063604 B
28	2.5	656	1	AU296144	AU296144 AU296144
29	2.5	660	5	BK602109	BK602109 BX602109
30	2.5	819	4	BI407957	BI407957 602918731
31	2.5	821	5	BP463227	BP463227 BP463227
32	2.5	844	5	BP170445	BP170445 BP170445
33	2.5	853	9	CR143596	CR143596 Reverse s
34	2.5	884	9	CNS039MA	AL452172 T. brucei
35	2.5	937	2	BF122575	BF122575 Tetradon
36	2.5	1033	5	BQ894385	BF122575 601761586
37	2.4	269	5	BP100096	BQ894385 AGENCOURT
38	2.4	273	4	BG952290	BP100096 BP100096
39	2.4	284	9	TA12H03P	BG952290 CM4-CT062
40	2.4	321	8	B27554	AL452172 T. brucei
41	2.4	350	1	BU609946	B27554 P20H3TFB IG
42	2.4	355	4	AV524543	BU609946 BU609946
43	2.4	360	9	BK894982	AV524543 AV524543
44	2.4	415	4	BI691463	BK894982 Arabidops
45	2.4	429	8	B27297	BI691463 603310916
46	2.4	449	2	BE809494	B27297 F2E23TR IGF
47	2.4	471	7	CN104206	BE809494 215061 MA
48	2.4	489	8	BH230880	CN104206 EC2CA25B
49	2.4	493	1	AV441702	BH230880 1006159H0
50	2.4	521	6	CB186427	AV441702 AV441702
51	2.4	526	6	CB259248	CB186427 TgESTzyf2
52	2.4	528	7	CN251799	CB259248 68-R01117
53	2.4	542	9	CC544615	CN251799 EST017730
54	2.4	544	1	AV554612	CC544615 CH240_426
55	2.4	549	2	A2833646	AV554612 AV554612
56	2.4	562	7	CF813383	A2833646 2M0115C23
57	2.4	581	6	CD217095	CF813383 NA413 GDN
58	2.4	610	4	BF607944	CD217095 TgESTzyf2
59	2.4	613	8	A2998423	BF607944 BU607944
60	2.4	621	5	BQ826796	A2998423 2M0285B23
61	2.4	621	7	CN253182	BQ826796 g47C04.x
62	2.4	627	4	BI159482	CN253182 EST019121
63	2.4	643	4	BJ606766	BI159482 602920296
64	2.4	656	7	CK118964	BJ606766 BJ606766
65	2.4	658	1	AV822322	CK118964 215618.D1
66	2.4	659	5	BX924334	AV822322 BX924332
67	2.4	660	6	CB469076	BX924334 BX924334
68	2.4	669	5	BX919629	CB469076 sn02_H02.
69	2.4	670	8	A2310918	BX919629 BX919629
70	2.4	688	4	BF591286	A2310918 1M0026A11
71	2.4	693	4	BI150046	BF591286 BU591286
72	2.4	715	2	BE038046	BI150046 602849459
73	2.4	716	9	AC391581	BE038046 AA08B12 A
74	2.4	724	4	BI105542	AC391581 Mus muscu
75	2.4	734	4	BI460985	BI105542 602891878
76	2.4	752	4	BI111057	BI460985 603204633
77	2.4	760	4	CL159077	BI111057 602899694
78	2.4	764	9	BI686089	CL159077 104_348.1
79	2.4	763	4	BI663982	BI686089 603313070
80	2.4	763	7	CO001622	BI663982 603288652
81	2.4	770	4	BI455983	CO001622 EST789992
82	2.4	776	4	BI155993	BI455983 603371761
83	2.4	796	2	BF163092	BI155993 602903527
84	2.4	806	4	BG918558	BF163092 601769608
85	2.4	806	5	BU057678	BG918558 602818331
86	2.4	806	5	BK920432	BU057678 UI-M-FRO-
87	2.4	841	8	B2755150	BK920432 BX920432
88	2.4	846	8	B2755150	B2755150 RUDSH04TB
89	2.4	859	4	BG919233	B2755150 PUFV797TD
90	2.4	865	4	BI661415	BG919233 602818064
91	2.4	875	9	CNS048B2	BI661415 603304708
92	2.4	886	7	CO001683	AL279188 Tetradon
93	2.4	890	4	BI686188	CO001683 EST990018
94	2.4	890	4	BI686188	BI686188 603313186
95	2.4	892	7	CO001682	BI686188 603318167
96	2.4	892	7	B2799630	CO001682 EST790017
97	2.4	917	4	BI663623	B2799630 PUFV797TB
					BI663623 603288331